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S

Title: Perfect score: US-09-830-647-2 1206 MNSGAMRIHSKGHFQGGIQV.....LKKPFVKVEDMSQSPAVHLM 234

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*

Database :

pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Ch Ch	Length	, 0	ID	Description
2 1	784 101.5	65.0 8.4	601 779	NN	T02633	hypothetical prote
انب	100.5		615		538088	٠,
4	94	7.8	1415		S52267	DNA polymeras
ъ	91		908		S51293	probable membrane
σı	91		994		A47474	NAD+ ADP-ribosyltr
7	90		219		C71927	islan
8	89	7.4	710		S26006	hypothetical prote
9	89	7.4	871		T48502	hypothetical prote
10	89	7.4	1119		B70126	
11	.7	7.3	392		B70242	conserved hypothet
12	7.	7.3	506		T28810	hypothetical prote
13	•		520		A71564	
14	7.	7.3	885		в69783	
15	87	7.2	426		F82315	
16	6.	7.2	690		T34149	hypothetical prote
17	86.5	7.2	1274		T02636	D1 protein homolog
18	6.		1462		T06819	topoiso
19	86	•	1081		T15692	hypothetical prote
20	85		273		E81330	probable periplasm
21	85	7.0	602		D69331	
22	85		773		T00502	
23	84.5		299		S34588	senescence marker
24	84.5		942		JC7316	
25	84.5	٠	1891		T13594	hypothetical prote
26	84.5		1920		T13893	gene hindsight
27	84		324		ω	probable phosphata
28	84		1059		A35210	ע
၁	83.5	א ס	2			ישווטאושמש (פר

hypothetical protein T14P8.6 - Arabidopsis thaliana
C;Specles: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Feb-2000
C;Accession: T01304
R;Kalicki, J.; Elliott, G.; Cloud, J.
R;Kalicki, J.; Elliott, G.; Cloud, J.
R;Kalicki, J.; Elliott, G.; Cloud, J.
R;Loscription: The EMBL Data Library, May 1998
A;Description: The sequence of A. thaliana T14P8.
A;Reference number: Z14290
A;Accession: T01304
A;Kolecule type: DNA
A;Residues: 1-779 < KAL>

ALIGNMENTS

A; Map position: 7 A; Map position: 7 A; Map position: 7 A; Map position: 7 A; Note: MUGSC:H_RG135C18.1 65.0%; Score 784; DB 2; Length 601; Best Local Similarity 100.0%; Pred. No. 3.1e-55; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 154; DB 2; Length 601; Mismatches 0; Indels 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 154; DB 2; Length 601; Mismatches 154; DB 2; Length	A; Map position: 7 A; Introns: 60/3; 77/3; 101/1; 126/3; 139/1; 154/A; A; Note: WUGSC:H_RG135C18.1 Query Match Best Local Similarity 100.0%; Pred. No. 3.1 Matches 154; Conservative 0; Mismatches Qy 74 RVEEFLSKDISYLISNKKEAKFAQTLGRISPVPSPESA [
A;Accession: T02633 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Moseidues: 1-601 <kel> A;Cross-references: EMBL:AC005164; NID:g3242749; PIDN:AAC23786.1; PID:g3242750</kel>	A;Accession: T02633 A;Status: preliminary; A;Molecule type: DNA A;Residues: 1-601 (KEL) A;Cross-references: EMB
RESULT 1 T02633 Typothetical protein RG135C18.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 05-Mar-1999 *sequence_revision 05-Mar-1999 *text_change 05-Nov-1999 C;Accession: T02633 R;Kellen, J.; Burkhart, J. Submitted to the EMBL Data Library, June 1998 A;Description: The sequence of Homo sapiens BAC clone RG135C18. A;Reference number: 214683	TO2633 hypothetical pr C;Species: Homo C;Date: 05-Mar- C;Accession: TO R;Kellen, J; B submitted to th A;Description: A;Reference num

```
hypothetical protein YKR019c - Yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Sate: 03-May-1994 #text_change 29-Oct-1999
C;Accession: S3808
R;Duesterhoeft, A.; Moestl, D.; Poehlmann, R.; Philippsen, P.
R;Duesterhoeft, A.; Moestl, D.; Poehlmann, R.; Philippsen, P.
A;Rcference number: S37811
A;Rcference number: S37811
A;Rcfession: S3808
A;Molecule type: DNA
A;Rcference type: DNA
A;Rcferences: EMBL:Z28244; NID:9486438; PID:9486439; GSPDB:GN00011; MIPS:YKR019c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YKR019c
A;Map position: 11R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193291
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 94/3; 202/3; 254/3; 562/3; 585/3; 610/2; 632/2; 667/1; 727/3
A;Note: T148.6
C;Superfamily: DNA mismatch repair protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 NGLLGIHSRSSSRNG---SNESLTPGQRTPDNRSQENLLTSFSSGRRLSSSSMEPATNKD 206
                                             385 NDTYDVYDDTDSDSESDQNQDALTKPRKRDRIKR---KIRNSANKTAHH 430
                                                                                                              184 KELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQSPAVH 232
                                                                                                                                                                               326 HLSSQYEMDASSEELGQHEQQPSMRFKTTLRKTSVSTNAENDHASSLHEGNLRYKY-NPS 384
                                                                                                                                                                                                                                            146 ----AIKDHDFIPS----NSILSNALSWGVKILHIDDIRYYIEQKK 183
                                                                                                                                                                                                                                                                                                            267 INQLSLCESEPSIASSNTTTT-TSNQGSGLPNLVPNYSSDMRKKKLVNKFKRKVFGSKPK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                          207 SNKALPKRRPSPPLQSSLVGSGQLHENENLSSISIDSRHSLNPDTSDVISNRSQTSLSQT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554 ADNVERHERVLGQFNLGFIIAKLERDLFIV 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ILHID------DIRYYIEQKKKELYLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 VLRNQTSSYRVEKSKFEVRALASRCLVEGDQLDDMVISKEDMTPSERDSELGNRISPGTQ 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AYTAETTSPHPSHDGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPS--NSILSNALSWGVK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 KVTDASKDLSSR-------SSFAQSTLNTFVTMGKRKHENISTILSETP 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 EKENPSLREVEIDNSSPMEKFKFEIKACGTKKGEGSLSVHDVTHLDKTPSKGLPQLNVTE 451
                                                                                                                                                                                                                                                                                                                                                                         99 LGRISPVPSPESAYTAETTSPHPSHDGSSFKS--PDTVCLSRGKLLVEK------ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 FYLDLPSVTISEKLQKDIKDLGGRVE------EFLSKDISYLISNKKEAKFAQT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 KLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQ-----TLGR-----ISPVPSPES 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 EKNRPSLKSLKTDNRP--EKSK-----CKPLWGK-----VFYLD-----LPSVTISE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SGAMRIHSKGHFQGGIQVKNEKNRPS------LKSLKTDNRPEKSKCKPLWGKV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.3%; Score 100.5; DB 2; Length 615; Similarity 20.8%; Pred. No. 2 4; B 2; Length 615; 60; Conservative 41; Mismatches 121; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 101.5;
22.9%; Pred. No. 2.7;
ative 35; Mismatches
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-908 <MAF>
A;Residues: 1-908 <MAF>
A;Cross-references: EMBL:Z46259; NID:g633655; PIDN:CAA86376.1; PID:g633664
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Galllardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63302
                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1 908 <NIC>
A;Residues: 1 908 <NIC>
A;Cross-references: EMBL:Z46259; NID:9633655; PID:9633664
A;Cross-references: EMBL:Z46259; NID:9633655; PID:9633664
A;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 1077-1085, 1995
Yeast 11, 1077-1085, 1995
A;Title: Sequencing analysis of a 24.7 kb fragment of yeast chromosome:
A;Reference number: S59562; MUID:96076632
A;Accession: S59562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein YNL321w - yeast (Saccharomyces cerevisiae)
W.Alternate names: hypothetical protein NO339
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1955 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S51293; S59562; S63302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Pacitti, D.F.; Barnes, M.H.; Li, D.; Brown, N.C. submitted to the EMBL Data Library, January 1995 A; Description: Staphylococcus aureus DNA polymerase III. A; Reference number: S52267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase III - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Decies: Staphylococcus aureus
C;Dete: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999
C;Date: 08-May-1995 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: Sequence analysis A; Reference number: S51285 A; Accession: S51293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, January 1995 A; Description: Sequence analysis of a 13.9 Kb fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 --- RLKKPFVKVEDMS--QSPA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           967 NFSGEYQPN-----AHNYTKVLFGEDKVFRAGTIGTVAEKTAFGYVKGYLNDQGIHKRGA 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 RYYIEQKKKELYLLKKSSTSVRDGGKRV-----GSGAQKTRTG------ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     915 SEFFNDGSVGSGFDLPDKTCETCGAPL----IKEGQDIPFEKFLGFK---GDKVPDI-DL 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 -----DGSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      858 ----GFAVIYLISQRLVKKSLDDGYLVGSRGSVGSSFVATMTEITEVNPLPPHYICPNCKT 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    805 VPIKDELYTPRMEGANEEIRELSYANARKLYGE----DLPQIVI-DRLEKELKSIIGN-- 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 7.8%; Score 94; DB 2; Length 1415;
Local Similarity 24.0%; Pred, No. 23;
hes 63; Conservative 34; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 EFLSKDISYLISN---KKEAKFAQTLGRISPVPSPESAYTAETT--SPHPSH------ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 IQVKNEKNRPSLKSLKTDNRP-EKSKCKPLWGKVFYLDLPSVTISEKLQKDIKDLGGRVE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment of yeast chromosome XIV identi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                 XIV identifies
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14;

7

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F;496-512/Domain: t
F;531-547/Domain: t
F;561-577/Domain: t
F;595-611/Domain: t
F;631-647/Domain: t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-908 <MAW>
A;Cross-references: EMBL:Z71597; NID:g1302433; PID:e239767; PID:g1302434; MIPS:YNL321w
A;Experimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-994 <UCH>
A; Residues: 1-994 <UCH>
A; Cross-references: GB:D13806; GB:D13807; GB:D13808; NID:g303545; PIDN:BAA02964.1; PID:g
A; Note: sequence extracted from NCBI backbone (NCBIN:129703, NCBIP:129704)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Uchida, K.; Hanai, S.; Ishikawa, K.; Ozawa, Y.; Uchida, M.; Sugimura, T.; Miwa, Proc. Natl. Acad. Sci. U.S.A. 90, 3481-3485, 1993
A;Title: Cloning of cDNA encoding Drosophila poly(ADP-ribose) polymerase: leucine A;Reference number: A47474; MUID:93234521
A;Accession: A47474
                                                                                                                                                                                                                                                                                                                  A;Cross-references: FlyBase:FBgn0010247
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase
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C: Keywords: transmembrane protein
F: 250-266/Domain: transmembrane #:
F: 413-429/Domain: transmembrane #:
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C;Accession: A47474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAD+ ADP-ribosyltransferase (EC 2.4.2.30) – fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;886-902/Domain:
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Best Local S
Matches 62
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                                            FEVKISENTIATISTELETQKKSTRMKFAEELGIHIVPIEFLDFVEADTEGAIKYINSTC
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                                                                                                                           KSTFSRSLLKTNKNNDVLVRPTIPRISP --- PLYNLKFSIIGLKNQHKELRKRIENLGGK 412
                                                                                                                                                                     KNEKNRPSLKSLKTDN---RPEKSKCKPLWGKVFYLDLPSVTIS---EKLQKDIKDLGGR 74
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                                                                                   VEEFLSKDISYLISNKKE-----AKFAQTLG-RISPV----
  -----PSPESAYTAETTSPHPSHD-----
                                                                                                                                                                                                                   Similarity
62; Conser
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---GSSFKSPDTVCLSRGKLLVEKAIKDHDF 152
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<TM10>
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4TM3>
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cag island protein - Helicobacter pylori (strain J99)
(;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: C71927
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
I'ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.;
Nature 397, 176-180, 1999
                                                                                                                                                                                        R;Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.; J. Mol. Biol. 223, 1-7, 1992
A;Title: Gene organization deduced from the complete sequence of liverwort Marchantia A;Reference number: S25941; MUID:92114051
A;Accession: S26006
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                                                        A; Cross-references: EMBL:M68929; NID:g786182; PIDN:AAC09460.1; PID:g786246 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, Fe
                                                                                                           A; Molecule type: DNA
A; Residues: 1-710 <ODA>
                                                                                                                                                                                                                                                                                                                                hypothetical protein - liverwort (Marchantia polymorpha) mitochondrion C;Species: mitochondrion Marchantia polymorpha C;Date: 07-May-1993 *sequence_revision 07-May-1993 *text_change 21-Jul-2000 C;Accession: S26006
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A; Residues: 1-219 < ARN>
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A; Genome: mitochondrion
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 ----YINLKKKE 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 ERKKDLEKEKKELLNKIEKQKIKHLERFILAGVKANIKENSFF-----LGCKNYPKCEWT
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nes 46; Conservative
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                                                                                                                                                                    translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
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C; Keywords: mitochondrion
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surface-located membrane protein 1 (lmpl) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 11-Jan-2000
C;Accession: B70126
R;Fraser, C.M.: Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra,
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A; Introns: 562/2; 602/3; 622/3
A; Note: F15N18.20
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A; Residues: 1-871 <BEV>
A; Cross-references: EMBL: AL163815
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                                                                                                                                                                                                                                246 KDY 248
                                                                                                                                                                                                                                                                                                                        186 EIPVDIMMEDVIKENVLKSQYDEVFPRDNVPFTDIIFPNDDLLHGNELSWDLEVSDLGET 245
                                                                                                                                                                                                                                                                               176 RYY 178
                                                                                                                                                                                                                                                                                                                                                                    141 -----SNALSWGVKILHIDDI 175
                                                                                                                                                                                                                                                                                                                                                                                                                126 KDDDSPKGKENIGTVETPVITQENTQSFQPASPASISVPVGEGTMSEMPTSVESSVQKDS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 DIKKDFDKIHHDL-LIKEMESVLR 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 DIRYYIEQKKKELYLLKKSSTSVR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 STVDKVVQSTLKELVEPHFESLFRDSSHGFRPGRSCHKALRDLRYSWTALTWLVQI---- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 KSPDTVCLSRGKLLVEKAIK-----DHDFIPSNSILS------NALSWGVKILHID 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 NVAPGIDGRTKADMTDKALEKLSKELRRQAYAPKP--AKRIIITKP----DGGSRPLSIA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 FFGSI-AKSAKATTKTKANKGESRP---VTPPALGRVFYEDIYNI---DNLRAGYKRLKG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 SNKKEAKFAQTLGRI-SPVPSPESAYTAETTSPH----PSHDGSSFKSPDTVCLSRGK-- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 KATOTESAPOK-PAKPYVNKKOHVPPPORSVKAMEEVNESVR---SKMRESLASALALVK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 KSLKTDNRPEKSKCKPLWGKVFYLDLP--SVTISEKLQKDIKDLGGRVEEFLSKDISYLI 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 FQGGIQVKNEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYLDLPSVTISEKLQKDIKDLGG 73
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37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.4%; Score 89; DB 2; Length 871; 20.2%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Mismatches 83; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Indels
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C;Genetics:
A;Genome: plasmid
C;Superfamily: Lyme disease spirochete plasmid conserved hypothetical protein BBG06
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conserved hypothetical protein BBI19 - Lyme disease spirochete plasmid I/1p28-4 ()Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: B70242 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; I son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzyberg, S.; Hanson, M.; Son, D.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, I Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, I A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Reference number: A70100; MUID:98065943
A;Accession: B70242
                                                                                                                                                                                                                    A;Cross-references: GB:AE000789; NID:g2690079; PIDN:AAC66184.1; PID:g2690081; TIGR:BB
A;Experimental source: strain B31
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A;Experimental source: strain B31
C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat
E;742-774/Domain: tetratricopeptide repeat homology *stabus atypical <TT1>
E;775-808/Domain: tetratricopeptide repeat homology <TT2-
F;809-842/Domain: tetratricopeptide repeat homology <TT4-
F;911-943/Domain: tetratricopeptide repeat homology <TT5-
F;911-943/Domain: tetratricopeptide repeat homology <TT5-
F;944-977/Domain: tetratricopeptide repeat homology <TT5-
                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-392 <KLE>
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Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: B70126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 LAQANKIQHLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTLAQANK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 LSWGVKILHIDDIRYYIEQ-KKKELYLLKKSSTSVRDGG---KRVGSGAQKTRTGRLKKP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 ----TAETTSPHPSHD-GSSFKSPDTVCLSRGKLLVEKAIKD-HDFI---PSNSILSNA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 TLGKNRLKELIKKGLSNKFQKVNELIENSKNKEASNLLLTLIKKDIEPNLINIPKDPYKK 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 NEKNRPSLKSLKTUNRPEKSKCKP---LWGKVF--YLDLPSVTISEKLQKDIKDLG---- 72
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1 Similarity 22.8%; Pred, No. 43;
58; Conservative 45; Mismatches 101; Indels
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Query Match

7.3%; Score 87.5;

DB 2;

Length 392

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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28810
A;Title: Genome sequence of
A;Reference number: A71570;
A;Accession: A71564
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, January 1996 A;Description: The sequence of C. elegans cosmid C54D1 A;Reference number: Z20527
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                                                                                                        R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell Science 282, 754-759, 1998
                                                                                                                                               hypothetical protein CT051 - Chlamydia trachomatis C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 C;Accession: A71564
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A; Introns: 78/2; 121/2;
C; Superfamily: aldehyde
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A; Residues: 1-506 <MIN>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 GSSFKSPDTVCLSRGKLLVEKAIKDHDFIPSNSILSNALSWGVKILHIDDIRYYIEQKKK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 VFYLDLP-----SVTISEKLQKDIKDLGGRVEEFLSKDISYLISNKKEAKFAQTLGRIS
                                                                                                                                                                                                                                                                                                                                                                                                                            TDLTKNKNKVCFKKKQKMLKEILSKTKKQLEKKGYDTKQLKLKIENIYKSYKTKPHFIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNNNKEEEEEDIRNNKIEKCQIKKYFNKCNFLSEEAKSILELNISKNKTIEIIKIIKKIE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEKNRPSLKSLKTDNRPEKSKCKPLWGKVFYL-----DLPSVTISEKLQKDIKDLGGRVE 76
                                                                                                                                                                                                                                                                                                                  TVGDPTTQVQIGAMNSKV---HYEKVKSYIELAKKEGADILCGGVTTIQNG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFLSKDISYLISNKKEAKFAQTLGRISPVPSP-----ESAYTAETTSPHPSHD 124
                                                                                                                                                                                                                                                                                                                                                                                                    ---NPGIVYSNYRKSDIASIARSSFLNQGEICLCTSRLFVQKPI-FADFVKSYVEEAKKF
                                                                                                                                                                                                                                                                                                                                                           -PSNSILSNALSWGYKILHIDDIRYYIEQKKKE-LYLLKKSSTSVRDG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180/3; 296/2; 332/3; 384/3; 421/3; 464/3 dehydrogenase (NAD+); aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%;
24.0%;
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                                                                 an obligate intracellular pathogen of MUID:99000809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 15; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87.5;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78;
                                                                                                                                                                  #text_change 15-Sep-2000
                                                                                                                                                                                                            (serotype D, strain UW3/Cx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 506
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                                                                                    humans: Chlamydia tra
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; May, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sakouchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchy T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil A; Accession: B69783
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C;Superfamily: Chlamydia trachomatis hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-520 <ARN>
A;Cross-references: GB.AE001279; GB:AE001273; NID:g3328434; PIDN:AAC67642.1; PID:g332
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be. C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter homolog ydgH - Bacillus subtilis
C; Species: Bacillus subtilis
                                                                                                                                                                                                                                                            A;Cross-references: GB:Z99106; GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12384.1; A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                    A; Residues: 1-885 < KUN>
                                                                                                                                                                                                                                                                                                                                            A; Molecule
                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: B69783
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 ANVTYLESKLKQPQRAFLSNTLPTE-----SSSSISLNGHI--PWLSTTNGSSSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 EKESPP---LSYNDL--PSVIKNSQFVVTQSQNKITGDLKMTNAQIANIKTPDTGDSNYA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 DKILNNDKLSTALNSATEVEKKIALAQKALGIEITINPDADTNPDTDQETPDPAPVADTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 --LISNKK------EAKFA---QTLG---RISPVPSPESAYTAETTSPHPSHDGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76
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9 HSKGHFQGGIQVKNEKNRPSLKSLKTDN-----RPEKSKCKPLWGKVFYLD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFKSPDTVCLSRGKLLVEKAIKDHDFIPSNS-----ILSNALSWGVKILHIDDIRY- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----YIEQKKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVEDMSQSPA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKDPREEDGFAEKTAEEQEQEIKEYNTKLAEYQKKIDDYNAAWEAFYSEAATVKYVKGIV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ISEKLQKDIKDLGGRVEEFLSKDISY-----
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                                                           1 Similarity 47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 21.9
65; Conservative
                                                                                   7,3%;
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                                                           30;
                                                        Score 87.5; D
Pred. No. 42;
30; Mismatches
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Pred. No. 21;
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                                                                                                             2:
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                                                        Gaps
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conserved hypothetical protein VCOSO3 [imported] - Vibrio cholerae (strain N16961 serogic) conserved hypothetical protein VCOSO3 [imported] - Vibrio cholerae (strain N16961 serogic) conserved hypothetical protein VCOSO3 [imported] - Vibrio cholerae (strain N16961 serogic) c. Species: Vibrio cholerae, Vibrio cho
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A;Molecule type: DNA
A;Residues: 1-426 <HEI>
A;Cross-references: GB:AE004136; GB:AE003852; NID:g9654921; PIDN:AAF93673.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0503
A;Map position: 1
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Search completed: December 27, 2001, 16:54:46 Job time: 276 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 --- SNSILSNALSWGVKILHID 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 YLISQSIL-----GILVYNVD 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 SPHPS--------DTVCLSRGKLLVEKAIKDHDFIPSNSILSNAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ISFKLAK-----GDVSAFLAEDGREYDRAGNSLERAFNR----YPV---DKAYRQITS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 VLVRNRPVDAM 385
                                                                                                                                                                                                                                                                                                                                                                                224 DMSQSPAVHLM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 VYKTRYLHLDKI------LVKKGQLVKRGQKIALAGA----TGRLTGPHLHFE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 SWGVKILHIDDIRYYIEQKKKELYLLKKSSTSVRDGGKRVGSGAQKTRTGRLKKPFVKVE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 GFNPKRKHPVTGRVVPHNGTDFATPIGAPVYSTGDGKVIV---VRKHPYAGNYLVIEHNS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ISEKLOKDIKDLGGRVEEFLSKDISYL--ISNKKEAKFAQTLGRISPVPSPESAYTAETT 117
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